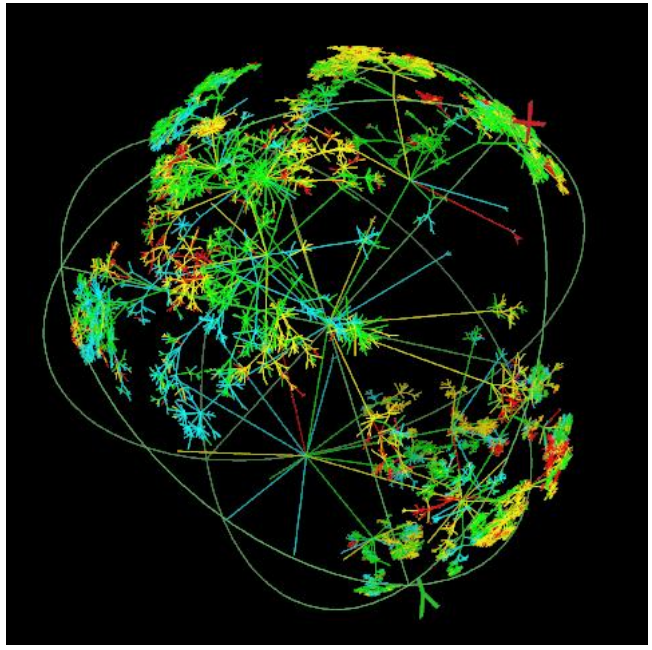
Small worlds and giant epidemics

Denis Mollison



14 May 2007

1 Introduction

Interests

- *Invasion* – threshold? R_0?

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- *Spread* – velocity / duration? final size?

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- *Spread* – velocity / duration? final size?
- *Persistence?* – pattern? control?

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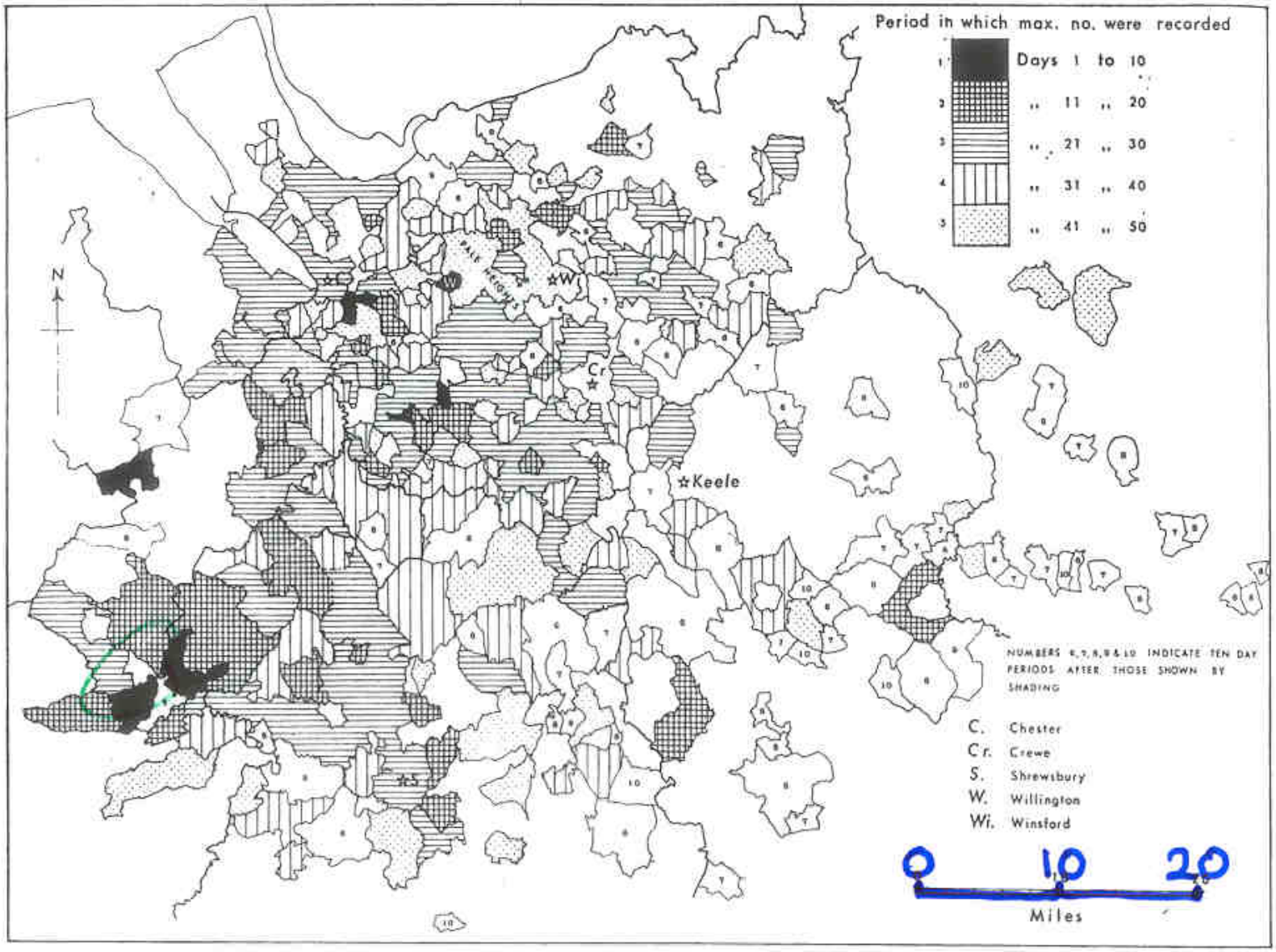
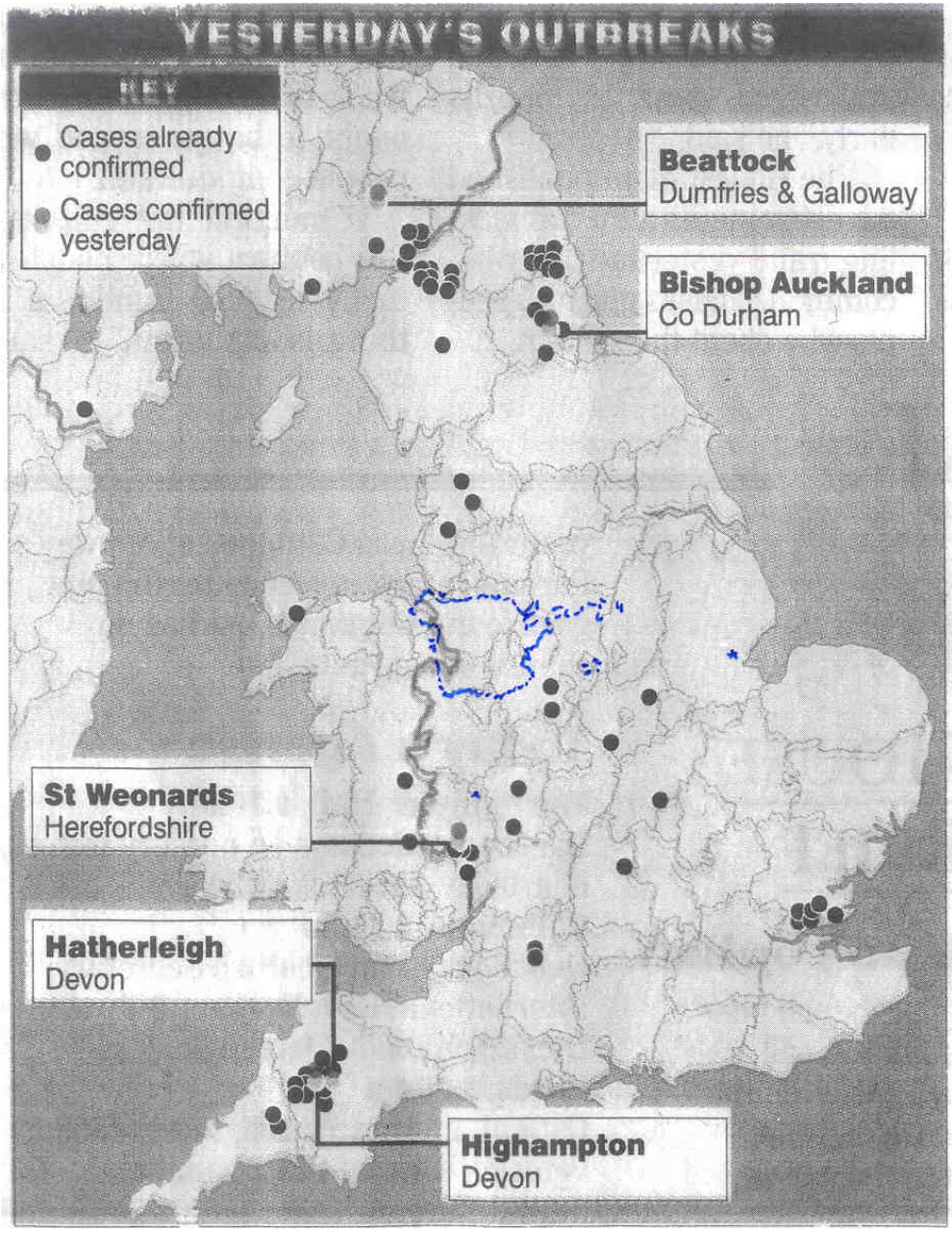
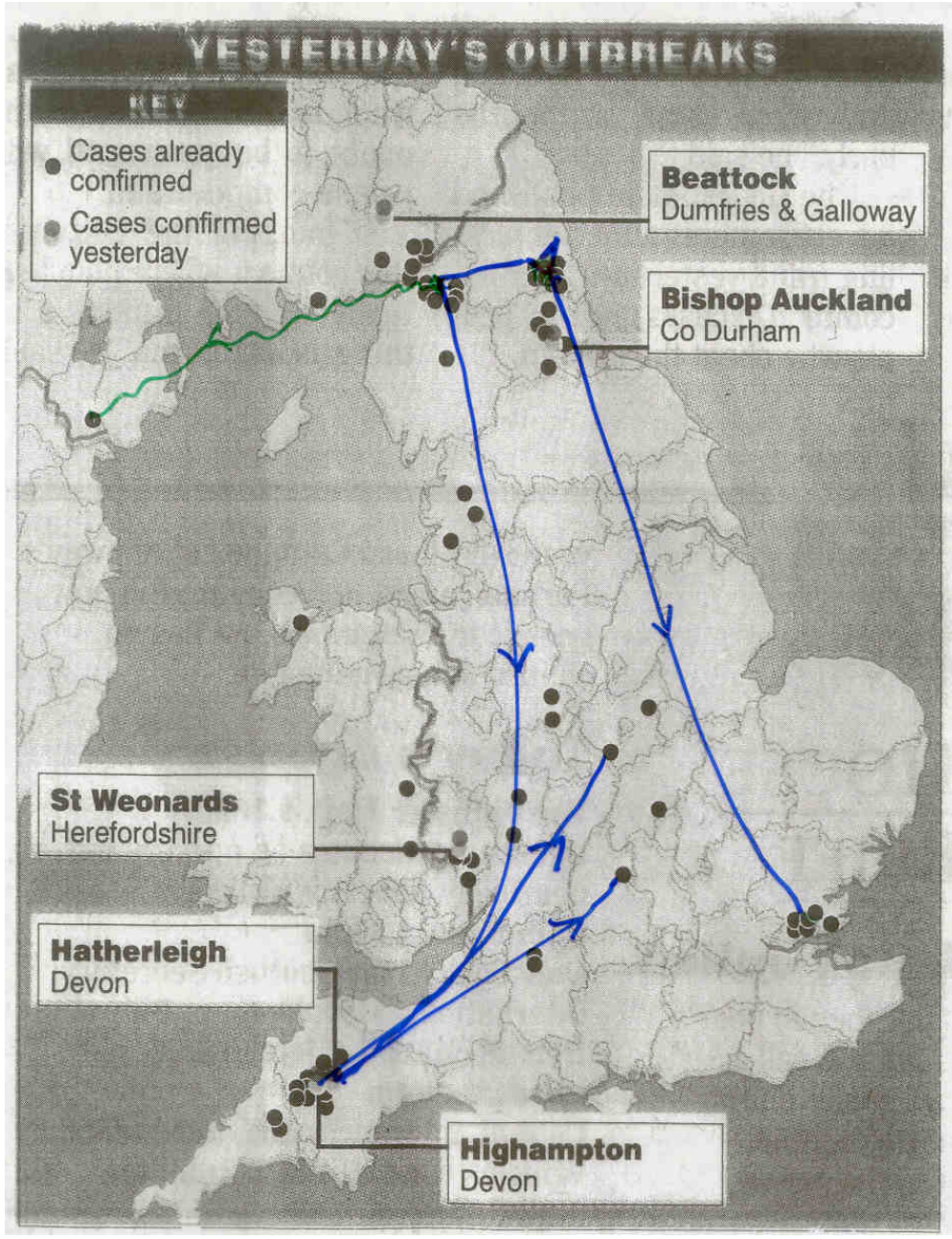
INTERESTS

- *Invasion* – threshold? R_0?
- *Spread* – velocity / duration? final size?
- *Persistence?* – pattern? control?

EXAMPLE Foot and mouth disease outbreaks in the UK, 1967-8 and 2001


Period in which max. no. were recorded
1
2
3
4
5
Days 1 to 10
" 11 " 20
" 21 " 30
" 31 " 40
" 41 " 50
N
HALE HEIGHTS
W
Wi
Cr
Keele
S
NUMBERS 6, 7, 8, 9 & 10 INDICATE TEN DAY PERIODS AFTER THOSE SHOWN BY SHADING
C. Chester
Cr. Crewe
S. Shrewsbury
W. Willington
Wi. Winsford
0 10 20
Miles


YESTERDAY'S OUTBREAKS
KEY
Cases already confirmed
Cases confirmed yesterday
Beattock
Dumfries & Galloway
Bishop Auckland
Co Durham
St Weonards
Herefordshire
Hatherleigh
Devon
Highampton
Devon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1967-8: spatial with jumps

2001: two phases

- global
- spatial with jumps

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2001: two phases

- global
- spatial with jumps

2003: SARS

2 Building models

Types

- individual or mass-action?
- stochastic or deterministic?

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Networks allow us to model the more realistic individual stochastic case.

Population space

- mean-field
- metapopulations
- spatial
- small-world

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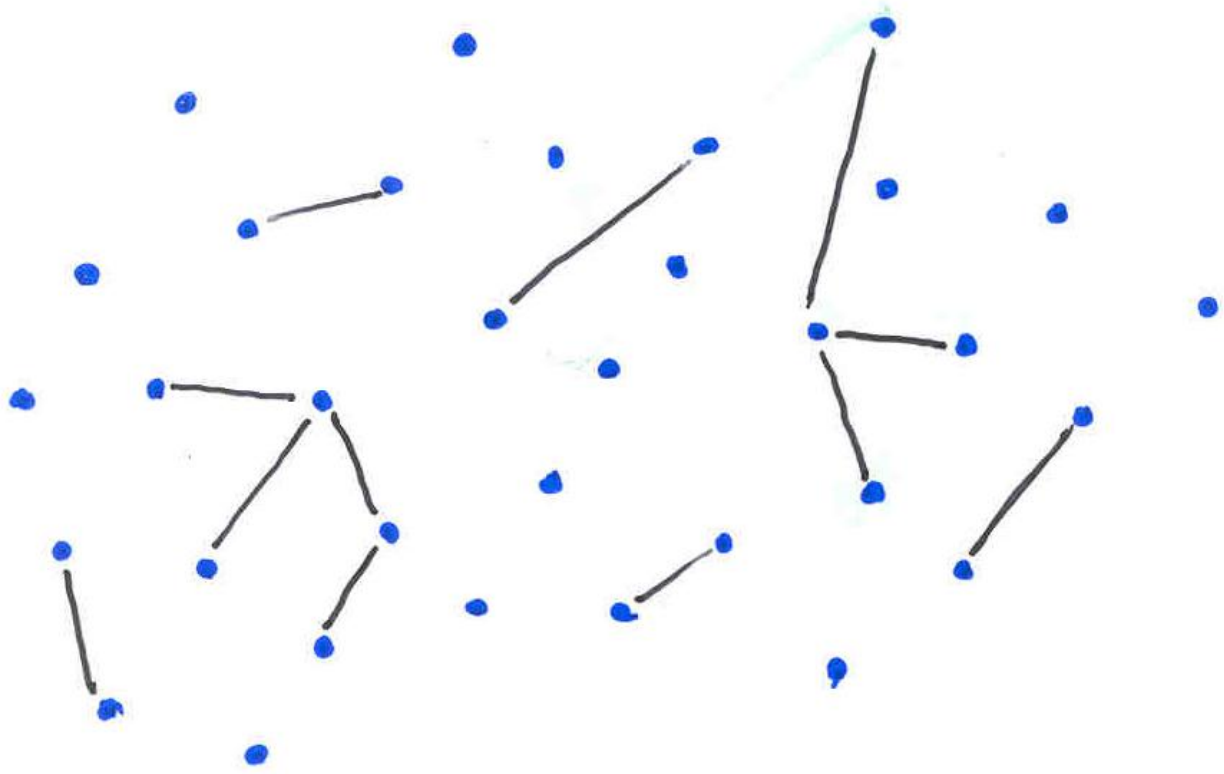
- spatial
- small-world

Shall look at examples of each

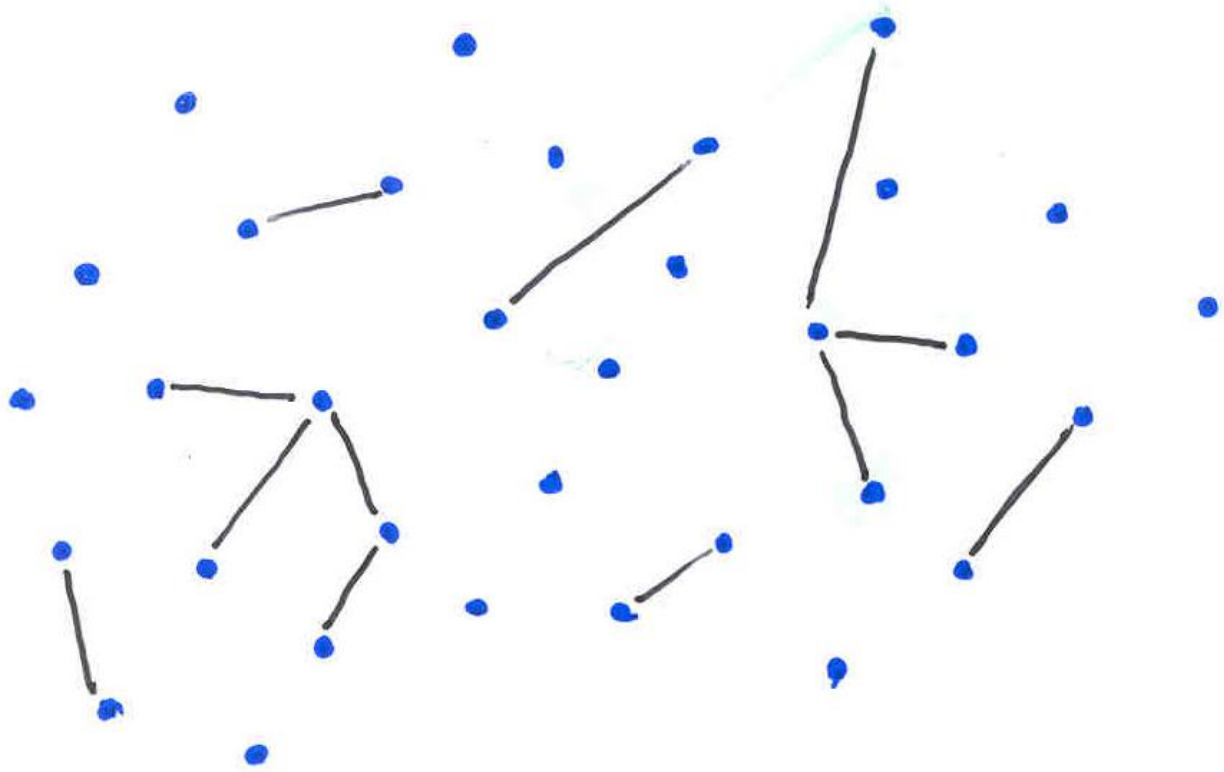
via random graph / network descriptions

Simple random graph



N individuals, each pair linked with probability p

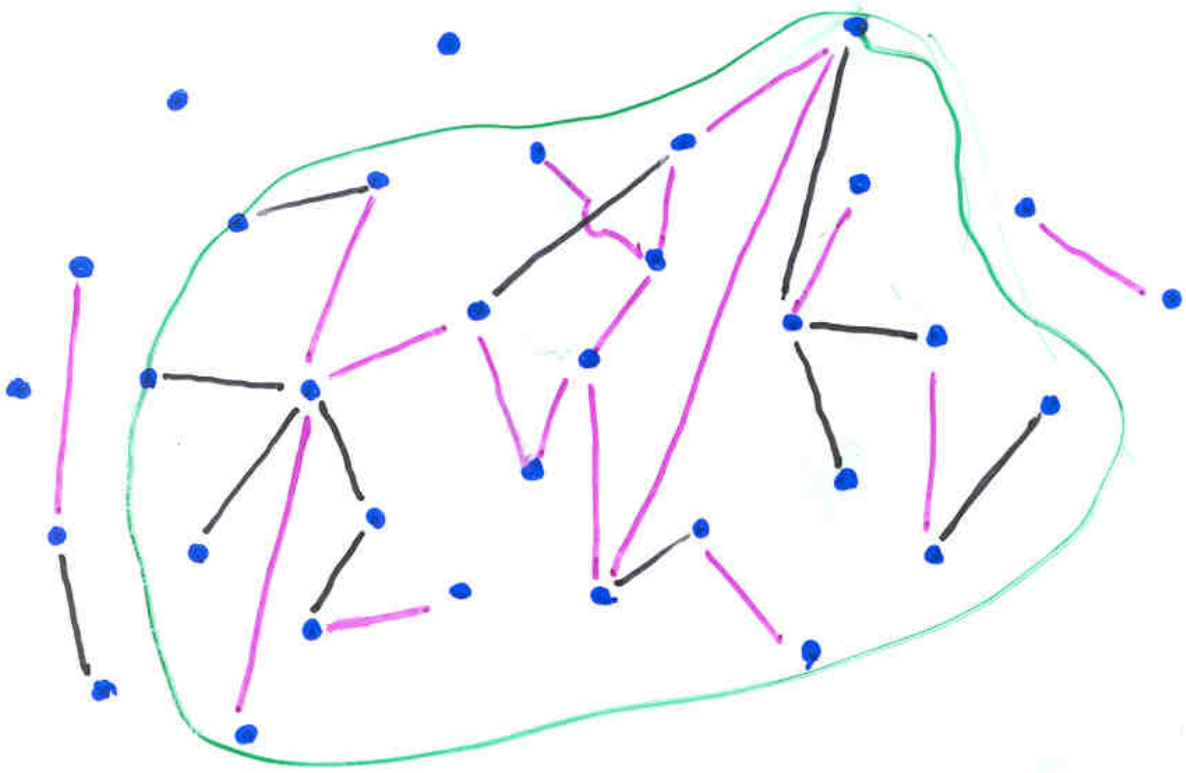
Simple random graph



Here $R_0 \equiv Np$ is < 1

R_0

The ***basic reproductive ratio*** of an epidemic is the mean number of new infections made by an infected individual in a mostly susceptible population



Here $R_0 \equiv Np$ is > 1

Results for simple random graph:

Giant component exists iff $R_0 > 1$.

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Diameter of giant, $T \sim \log N$.

Results for simple random graph:

Giant component exists iff $R_0 > 1$.

Diameter of giant, $T \sim \log N$.

Final size (and probability of a large outbreak) are both given by the largest solution of

$$z = 1 - \exp(-R_0 z)$$

Deterministic mass-action equivalent,

a differential equation model ('SIR'):

$$\begin{aligned} \dot{S} &= -cSI \\ \dot{I} &= cSI - dI \\ \dot{R} &= dI \end{aligned}$$

Results for 'SIR':

Large outbreak *always* occurs if $R_0 \equiv c/d > 1$,

duration $T \sim \log N$,

and the final size z is given by

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Structural choices for network models

- Directed or undirected?
- Degree – fixed? Poisson? 'scale-free'?
- Large-scale structure
  (mean-field to spatial)

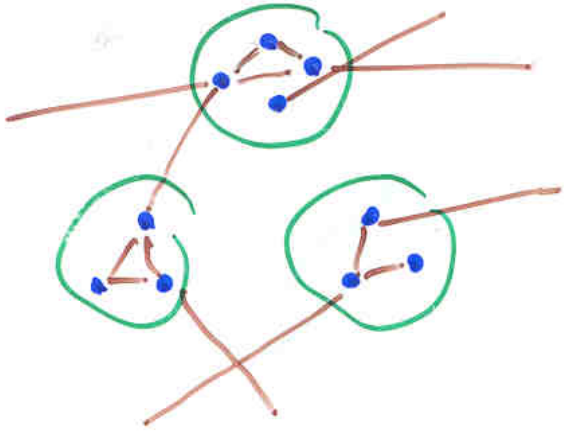
Note The case of Poisson degree is special – it corresponds to independence among an individual's contacts, allowing use of the *undirected* Simple Random Graph as a model

Note Should in and out links be independent?

For undirected graphs, they are only independent in the SRG case. For any other degree distribution, the effective mean number of contacts is 'size-biased'.

Example: the 'scale-free' case, with $p_n \sim n^{-3}$, has $R_0 = \infty$.

3 Metapopulation models



3.1 Context

Applications

- *household / group* – *e.g.* flu, measles
- *neighbour / long distance* – *e.g.* North Sea seal epidemics

3.2 Cases of interest

Pre-specified groups

m groups of size n, $\quad N = mn$

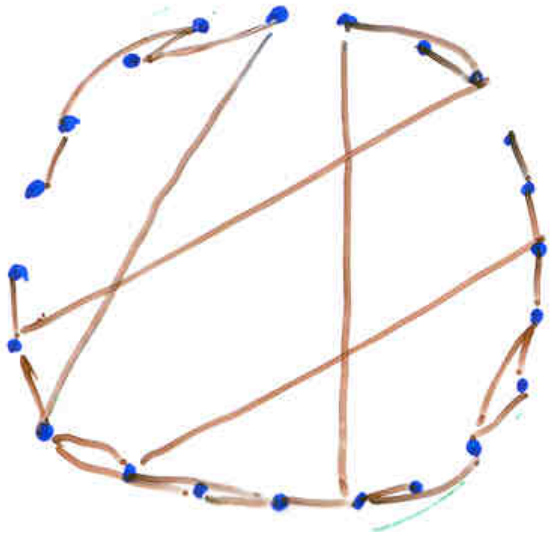
- n large (Watson 1972)
- m large – 'households'
- m and n large – 'epidemics among giants'
- variable group size, *e.g.* households of sizes $n_i \quad (1 \leq i \leq m)$

Theory

- *household / group* – previously treated as 'local + external' (*e.g.* Becker 1979)
- *other cases* – not previously treated. Can extend ideas used in the homogeneous mixing case:
  - random graphs
  - Sellke construction
  - *etc.*

Groups determined by a local process

e.g. ***'Great circle' epidemic***



For the great circle, local contacts produce connected components with size distribution given by

$$\pi_k^\star = kp^{k-1}(1-p)^2$$

Note : $\pi_k^\star = \mathrm{P}(\text{an individual belongs to a group of size } k)$

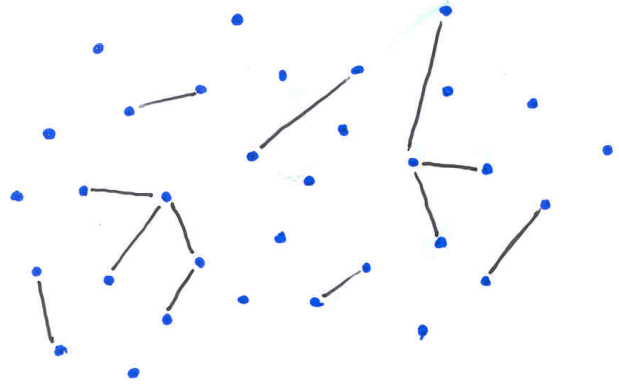
Unified approach

Whichever case we have, if we think of local contacts first, these in both cases determine a 'realised local structure', which we can think of as pre-determined when we go on to consider global contacts.

3.3 Amplification

Consider first the process including only global contacts, with reproductive ratio $R_0 = Nq$.

Relative to this 'global-only' process, local contacts have an amplifying effect. If we infect one individual in a local clump this results in global contacts from all members of the clump.



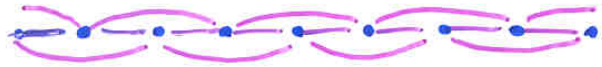
Hence the overall reproductive ratio is

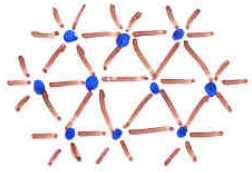
$$R_T = R_0 \mu$$

where μ is the mean size of component to which a random individual belongs.

- Generalizes to directed graphs, and to more levels of mixing
- $R_T >> R_0$ when local groups are both large and above threshold

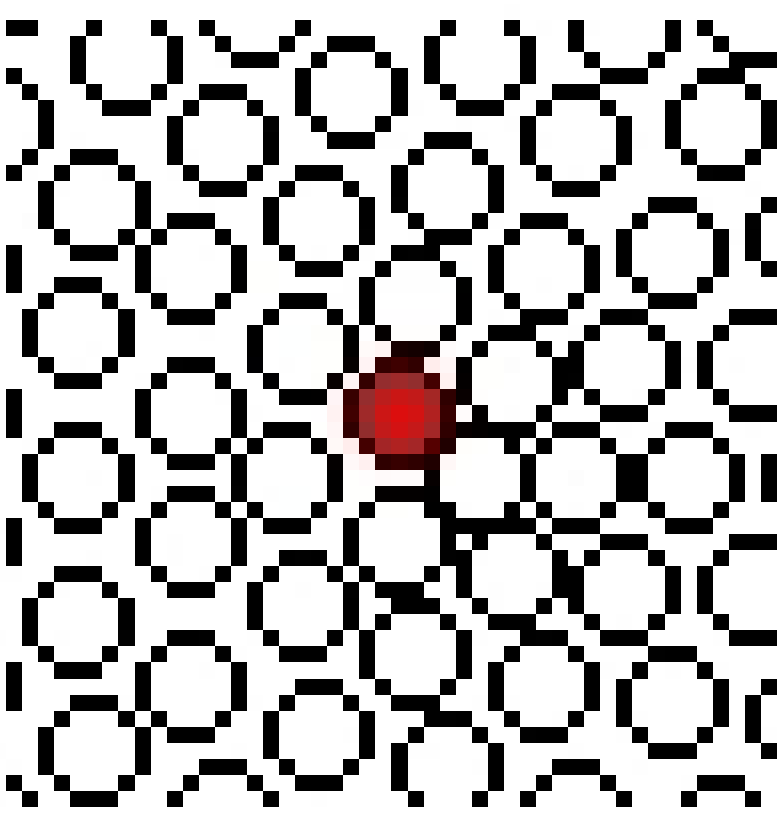
4 Spatial models



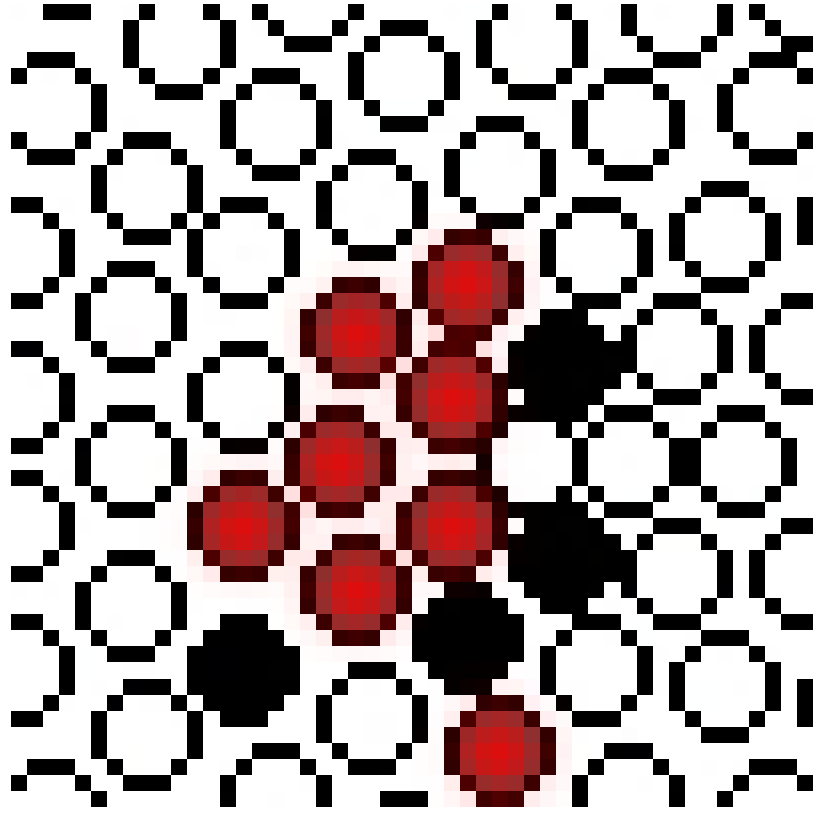


Nearest-neighbour

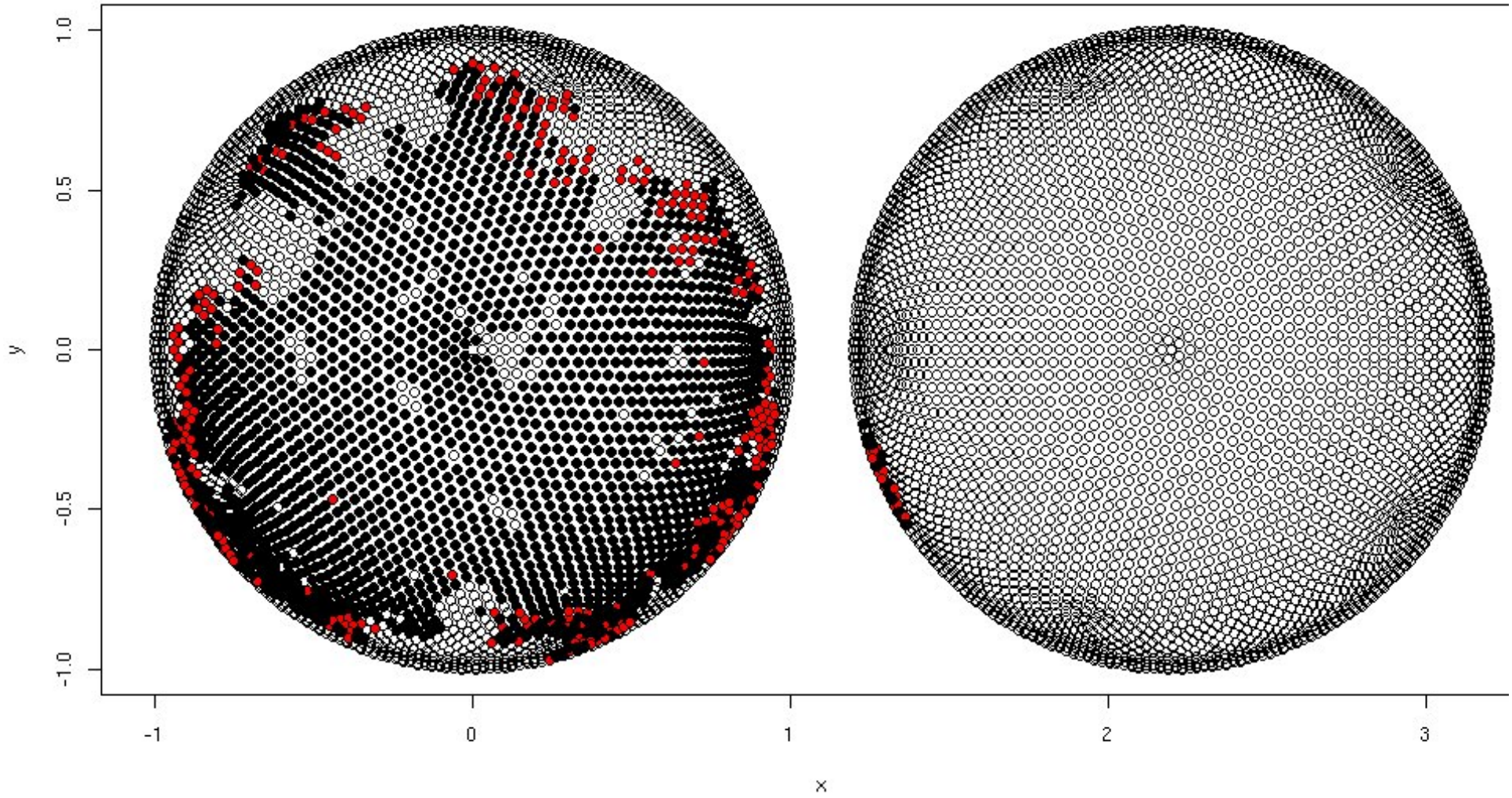
. . . or more general dispersal distribution

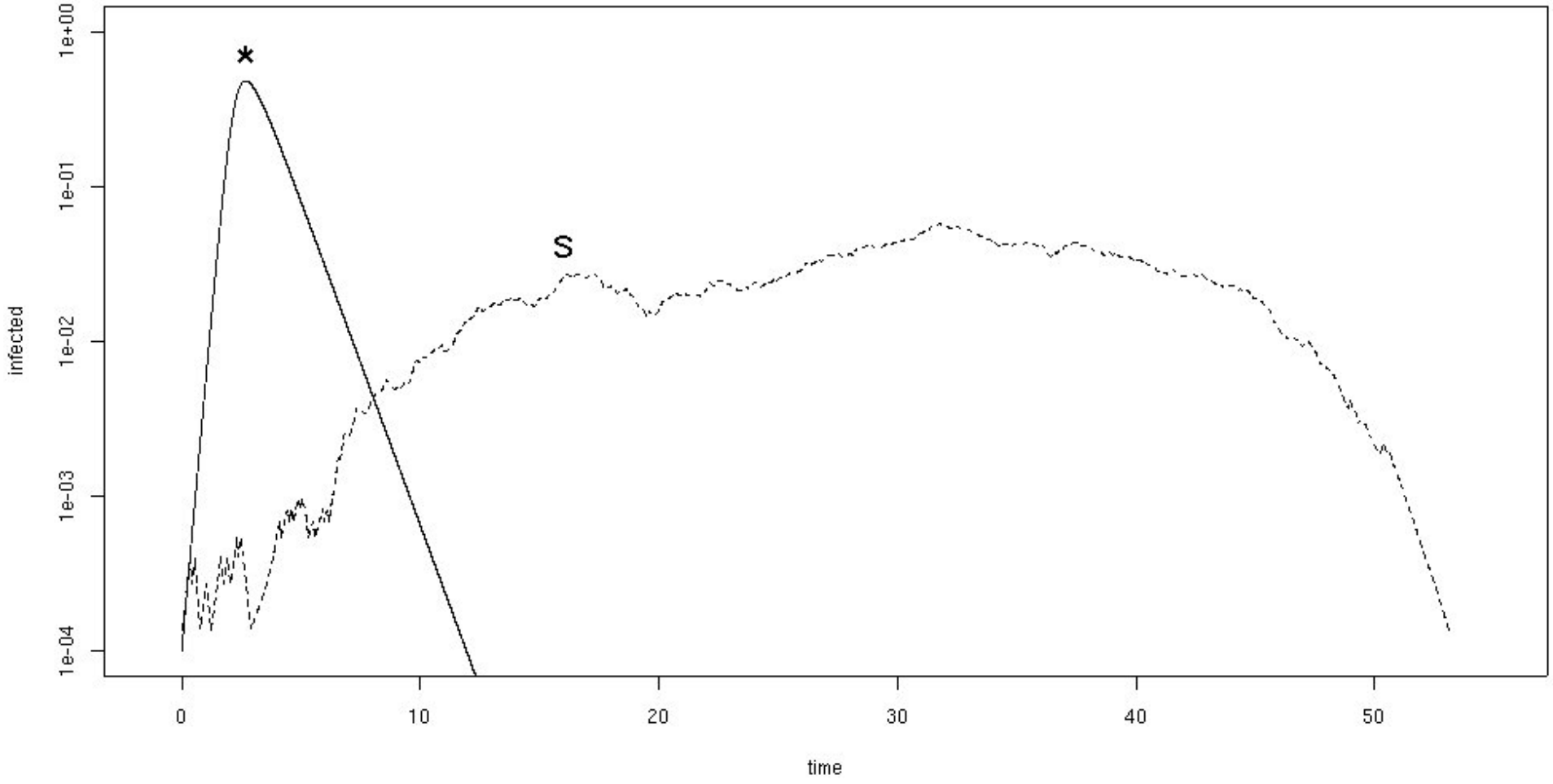


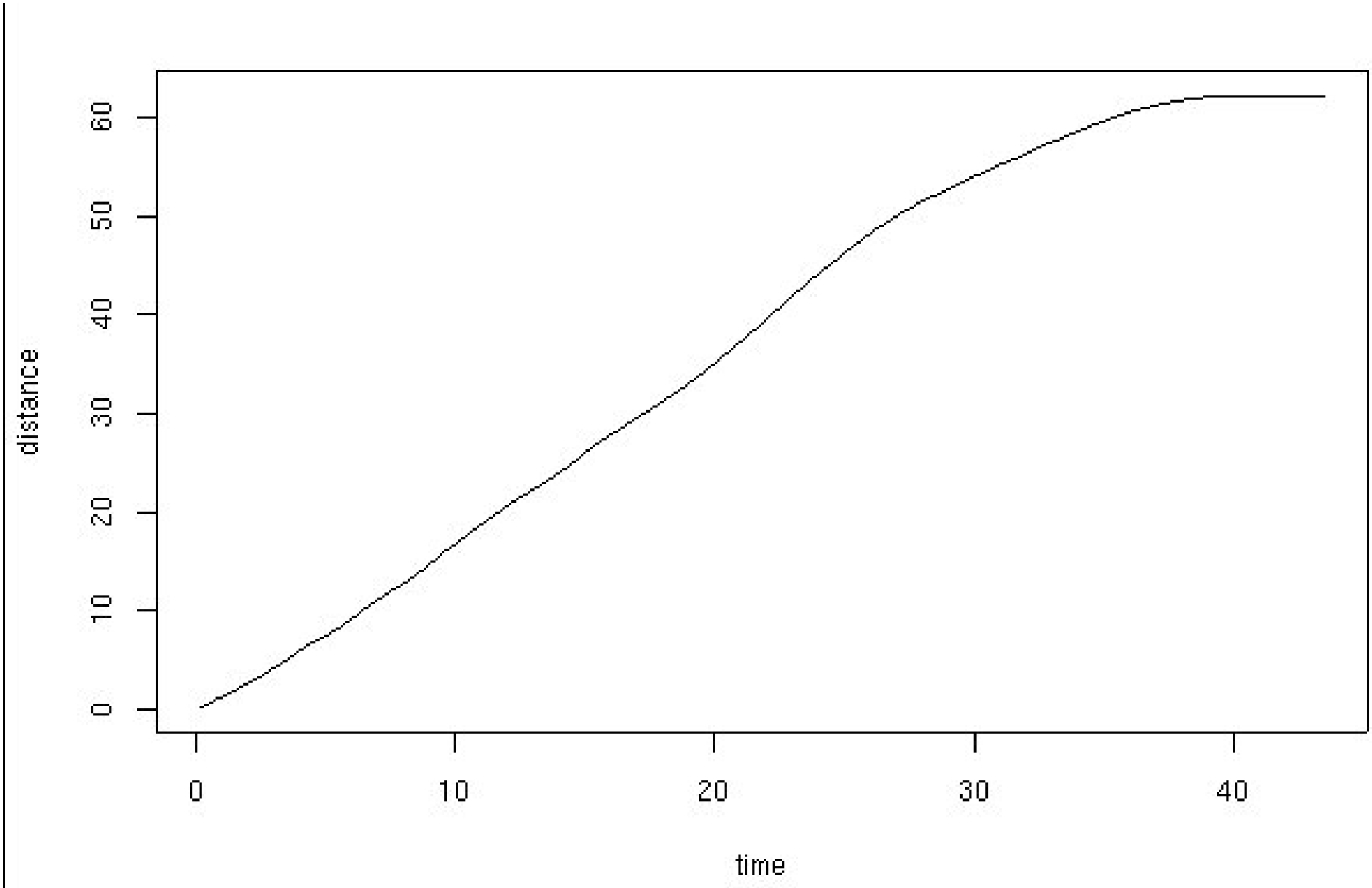
Time 0



Time 1


1.0
0.5
0.0
-0.5
-1.0
y
-1
0
1
2
3
x


infected
1e+00
1e-01
1e-02
1e-03
1e-04
*
S
0
10
20
30
40
50
time

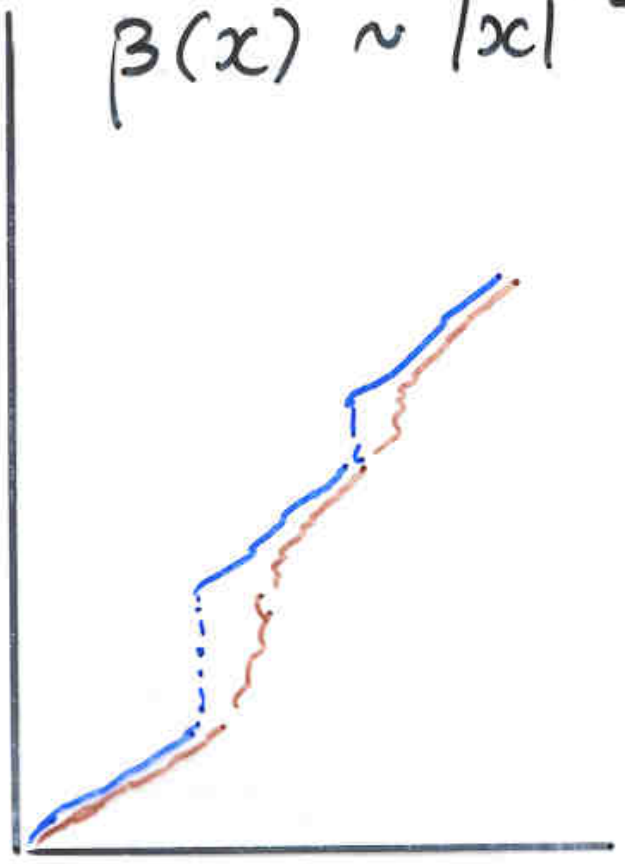

distance
0
10
20
30
40
50
60
0
10
20
30
40
time

Velocities of stochastic spatial models are hard to calculate.

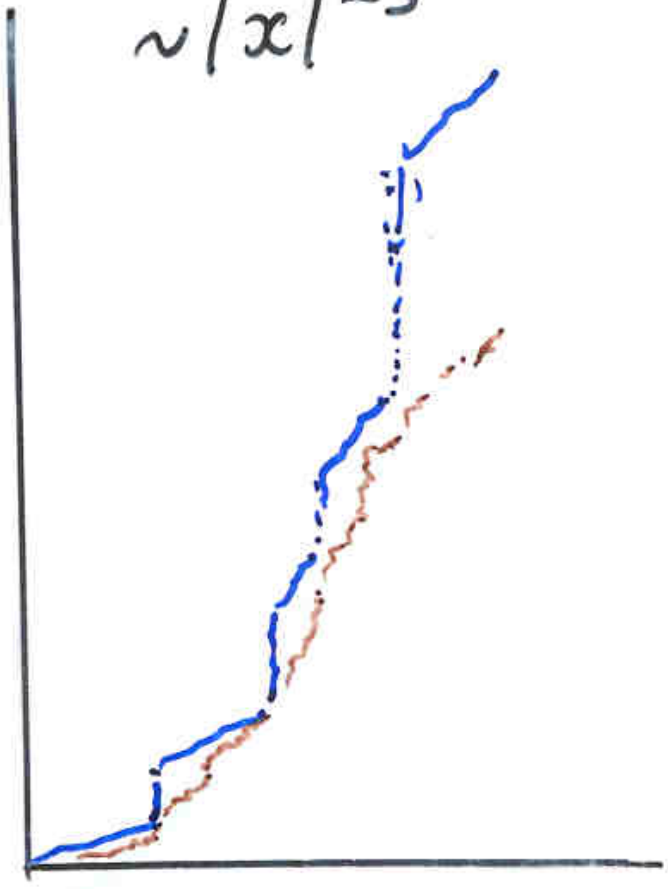
It is known that stochastic and deterministic nonlinear models have qualitatively different conditions for finite velocity:

- Deterministic case: probability of long-distance contact must fall off at least exponentially.
- Stochastic case: only require finite variance

$\beta(x) \sim |x|^{-4}$



$\sim |x|^{-3}$



Approximations using deterministic models

Provided the dispersal distribution falls off at least exponentially, spatial deterministic models do provide reasonable approximations.

Many examples have been studied, especially diffusion equations (KPP, Fisher, Skellam, ...)

Breakthrough in late 1980s: the R&D kernel approach of Diekmann (and others) shows how linear theory can find velocities for a wide range of nonlinear models.

All you need is the *reproduction and dispersal* kernel K that describes the space-time distribution of the infections made by an individual in a mostly susceptible population.

Breakthrough in late 1980s: the R&D kernel approach of Diekmann (and others) shows how linear theory can find velocities for a wide range of nonlinear models.

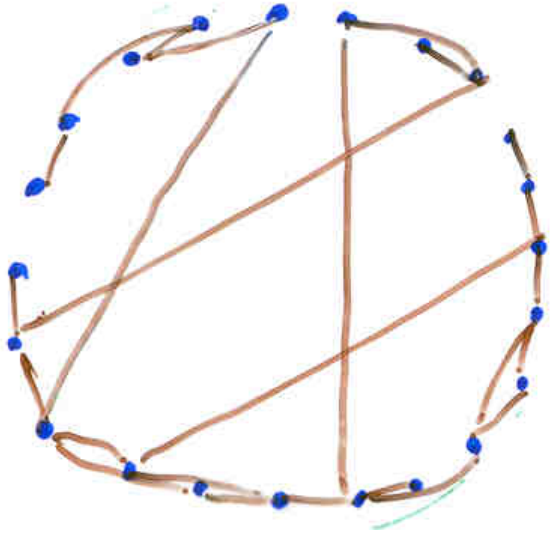
All you need is the *reproduction and dispersal* kernel K that describes the space-time distribution of the infections made by an individual in a mostly susceptible population.

Can think of K as a space-time version of R_0

Three advantages of the R&D kernel approach:

- Much easier to calculate
- Not restricted to DEs and diffusion equations
- Can look at the broad dependence of the velocity on basic components
  (*e.g.* is it $\sim \log(R_0)$, $\sim \sqrt{R_0}$ or $\sim R_0$?)

5 Small worlds



Threshold: $R_T = R_0\mu > 1$ (as for metapopulation model)

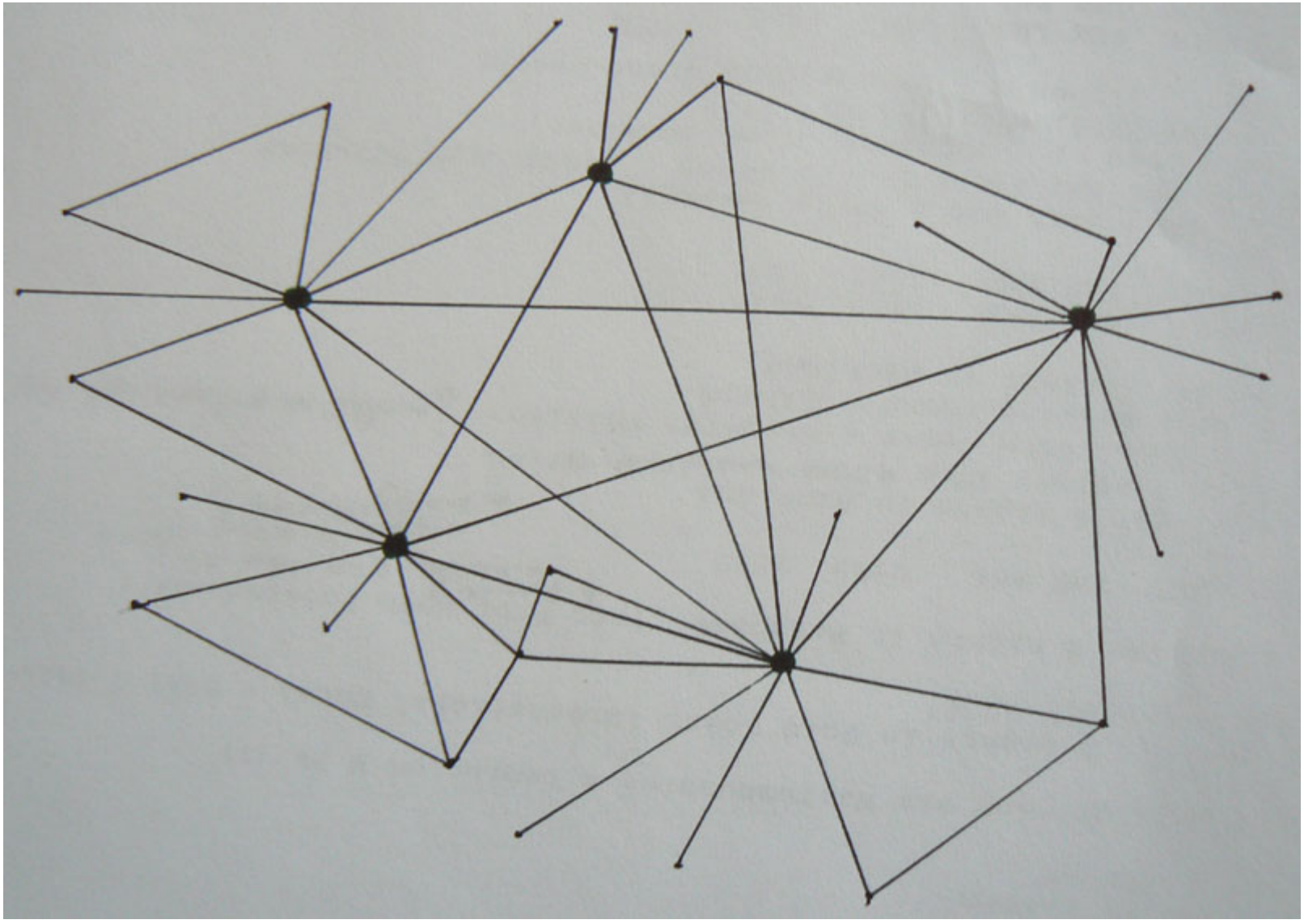
T reduces from $\sim N$ to $\sim \log N$ as the number of global links increases

‘Small world’ phenomenon:

The proportion of global links required to reduce T to $\sim \log N$ is surprisingly small.

‘Scale-free’ models:

A related study is of models with very high variability in the number of contacts per individual.



$T = 3$

DARWIN
TIMOR SEA
INDIAN OCEAN
KUNUNURRA
KIMBERLEY
BROOME
CANNING BASIN
PORT HEDLAND
KARRATHA
PILBARA
GREAT SANDY DESERT
PARABURDOO
NEWMAN
ALICE SPRINGS
WESTERN AUSTRALIA
AYERS ROCK/ ULURU
KALGOORLIE
NULLARBOR PLAIN
PERTH
Great Australian Bight
ADELAIDE
MT ISA
CAIRNS
TOWNSVILLE
QUEENSLAND
BRISBANE
GOLD COAST
SYDNEY
NEW SOUTH WALES
CANBERRA
MELBOURNE
VICTORIA
HOBART
TASMANIA
SOUTH PACIFIC OCEAN
CORAL SEA
TASMAN SEA
Sector times and distances may vary according to seasonal weather, flying conditions, aircraft type and route variations. Routes shown are indicative only.
Location of The Qantas Clubs or associated lounges
Qantas routes
Jetstar routes
QantasLink routes
Routes operated by other airlines for Qantas
International Gateway Port
National Capital
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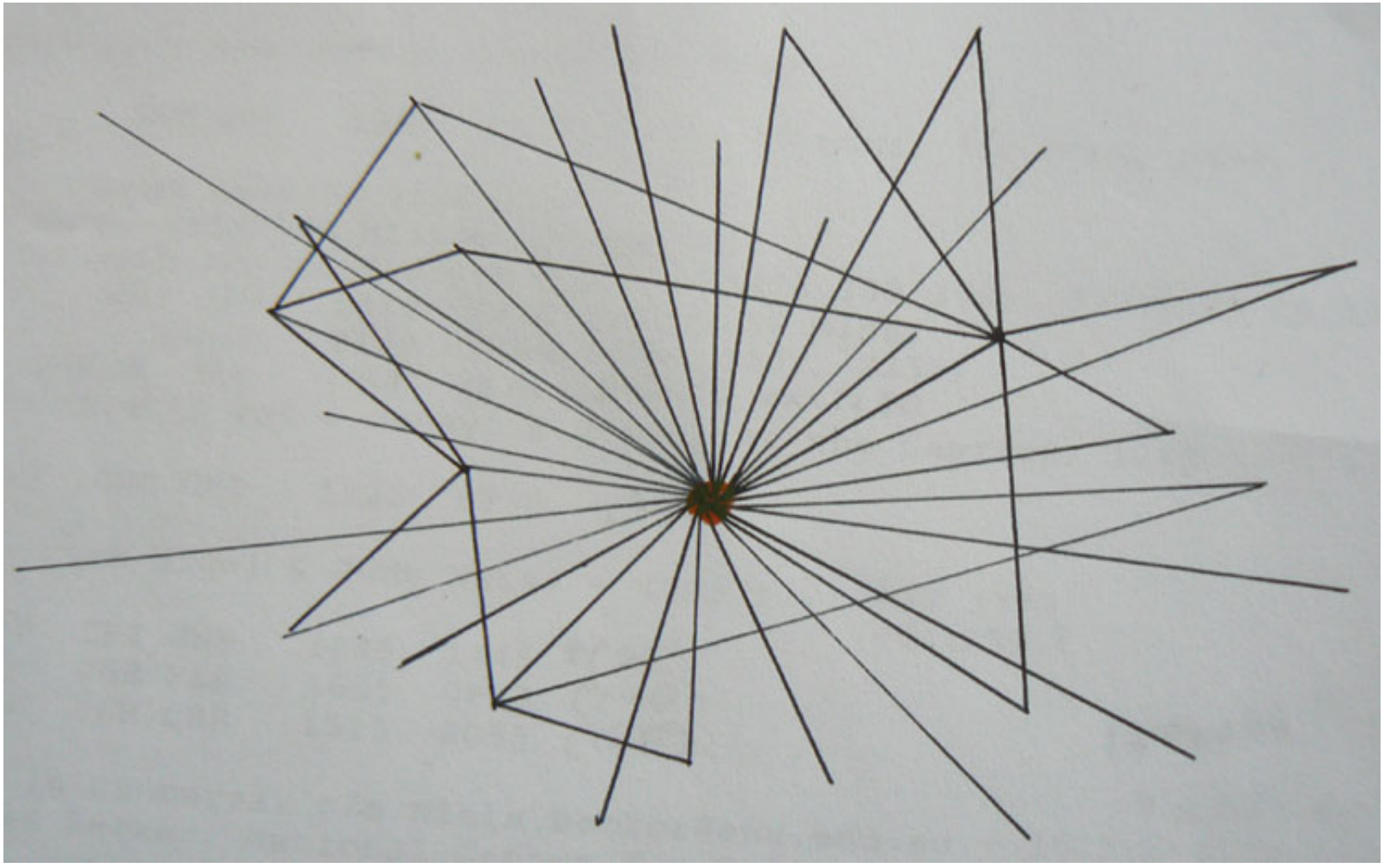
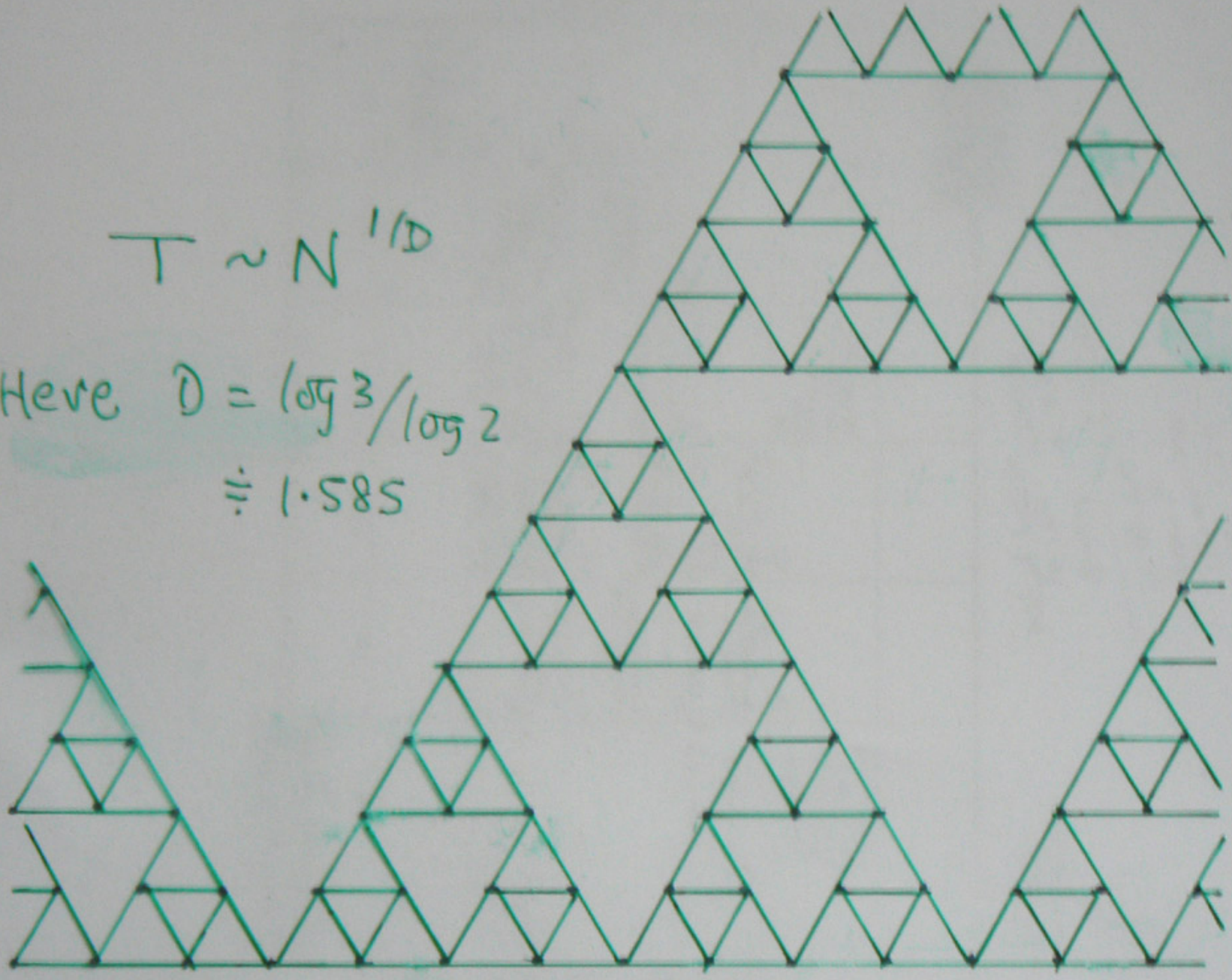


$T = 2$

$T \sim N^{1/D}$

Here $D = \log 3 / \log 2$

$\doteqdot 1.585$



6 Two recent examples

Pair approximations to spatial models

In 2001, two British groups attempted real-time modelling and prediction of the Foot-and-mouth epidemic.

A Cambridge-based group used a spatial micro-simulation.

The other group used a *pair approximation* to avoid the difficulties and complexities of a fully spatial model.

Pair approximations

Reconsider the deterministic SIR:

$$\begin{aligned} \dot{S} &= -cSI \\ \dot{I} &= cSI - dI \\ \dot{R} &= dI \end{aligned}$$

More accurately

$$\begin{aligned}
\dot{S} &= -c[SI] \\
\dot{I} &= c[SI] - dI \\
\dot{R} &= dI
\end{aligned}$$

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\begin{aligned}
\dot{S} &= -c[SI] \\
\dot{I} &= c[SI] - dI \\
\dot{R} &= dI
\end{aligned}
$$

$$
\begin{aligned}
[\dot{SS}] &= -2c[SSI] \\
[\dot{SI}] &= c([SSI] - [SI] - [ISI]) - d[SI] \\
[\dot{SR}] &= \cdots \\
[\dot{II}] &= \cdots
\end{aligned}
$$

For closure, use

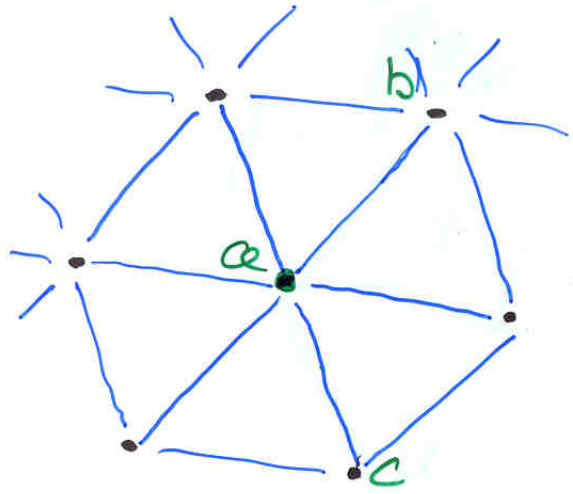
$$[ABC] \approx (1-\frac{1}{n})\frac{[AB][BC]}{[B]} \times(1-\phi+\phi\frac{[AC]}{[A][C]})$$

where the clustering parameter ϕ is

$$P(ac|ab\ \&\ bc)$$

(Keeling 1999)

EXAMPLE hexagonal lattices (HBFs)

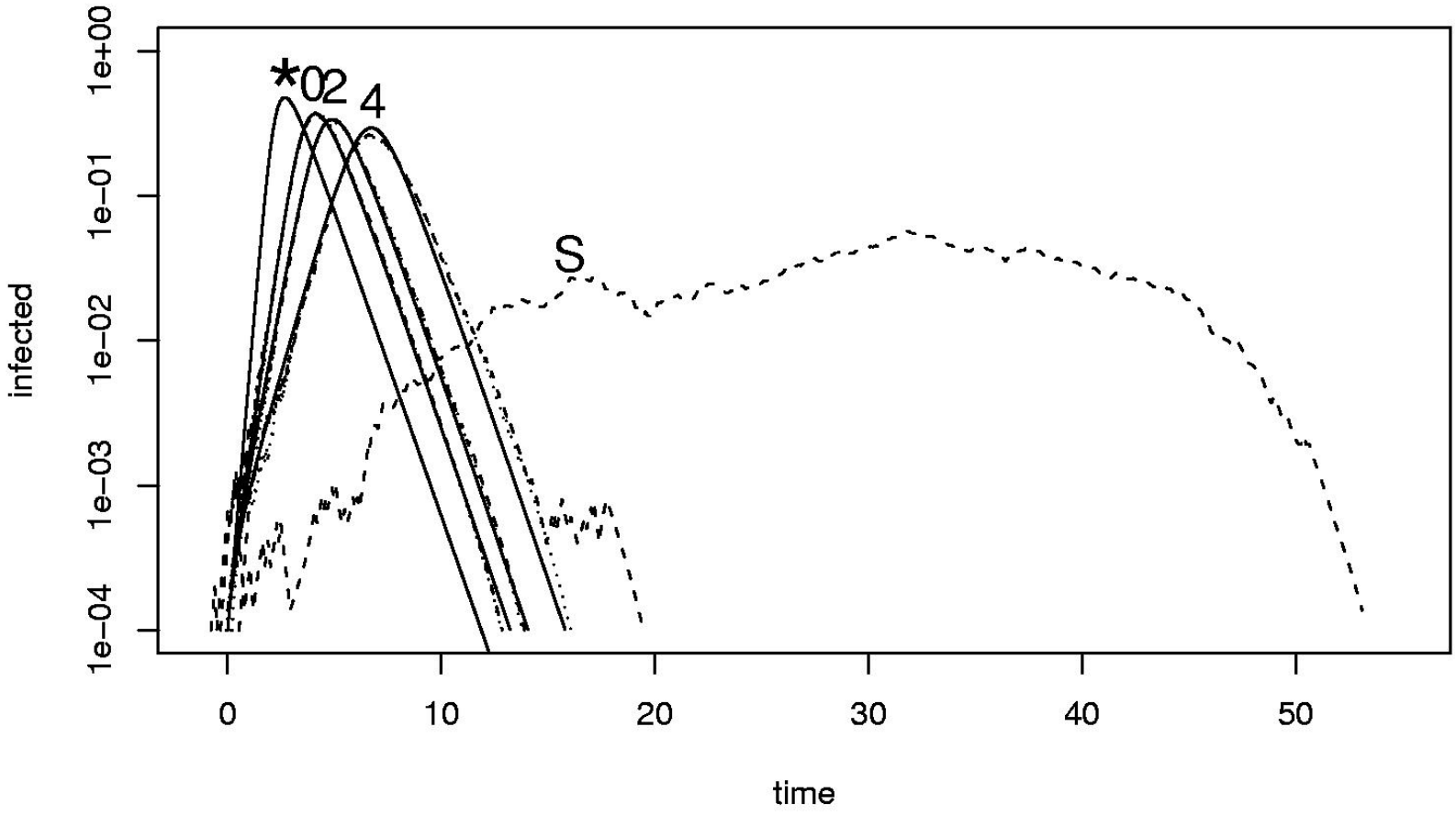


$\phi = 6/15 = 0.4$

So does $G(6, 0.4)$, the random graph with degree 6 and clustering parameter $\phi = 0.4$, have $T \sim \sqrt{N}$?

SIR (dashed line) and its pair approximation (solid line), for $\phi = 0$, 0.2, 0.4.

Also, spatial SIR ('S') and ordinary deterministic SIR ('$\star$').



We conclude that local structure is a poor guide to global structure.

The pair approx is good for 'typical' $G(6, \phi)$ graphs, but such graphs are much closer to mean-field – with $T \sim \log N$ – than spatial.

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The pair approx is good for 'typical' $G(6, \phi)$ graphs, but such graphs are much closer to mean-field – with $T \sim \log N$ – than spatial.

Yet there *are* spatial examples of $G(6, \phi)$ – HBFs – with $T \sim \sqrt{N}$!

The resolution of this paradox is that the non-mean-field cases are of negligible probability –

HBFs, even as small as $N = 150$,
are *Adams-improbable*.

‘We are now cruising at a level of $2^{25,000}$ to 1 against and falling, and we will be restoring normality just as soon as we are sure what is normal anyway.’

(Adams 1979)

Badgers and cattle TB

A cause of major controversy in Britain since the 1970s.

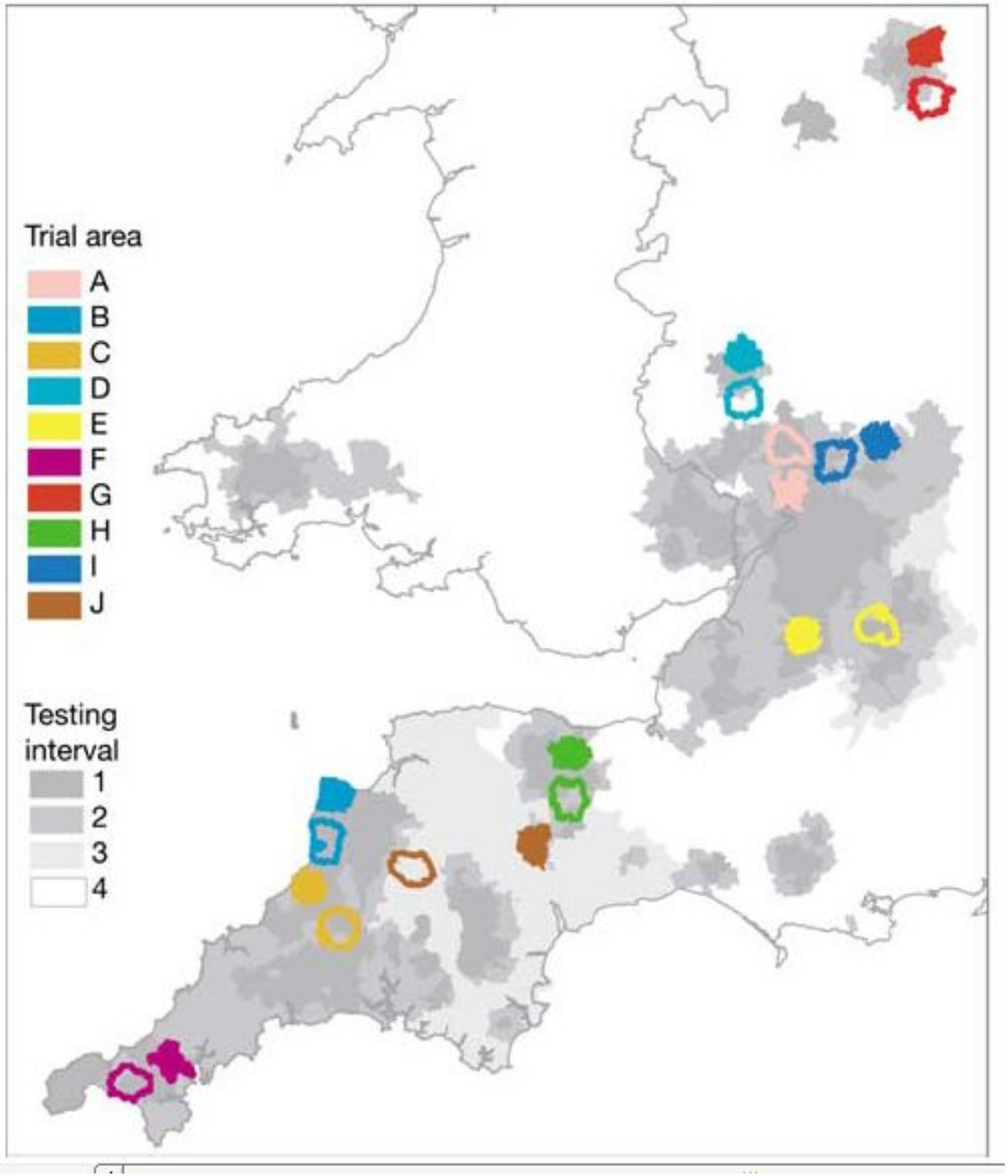
The Krebs Report (1997) proposed, among other things,

Badgers and cattle TB

A cause of major controversy in Britain since the 1970s.

The Krebs Report (1997) proposed, among other things, an experiment (!), with 10 sets of 3 areas, to compare three strategies:

- proactive
- reactive
- survey only


Trial area
A
B
C
D
E
F
G
H
I
J
Testing interval
1
2
3
4

The reactive part of the experiment was stopped in 2003, because it was making TB incidence significantly worse (estimated effect: +30%).

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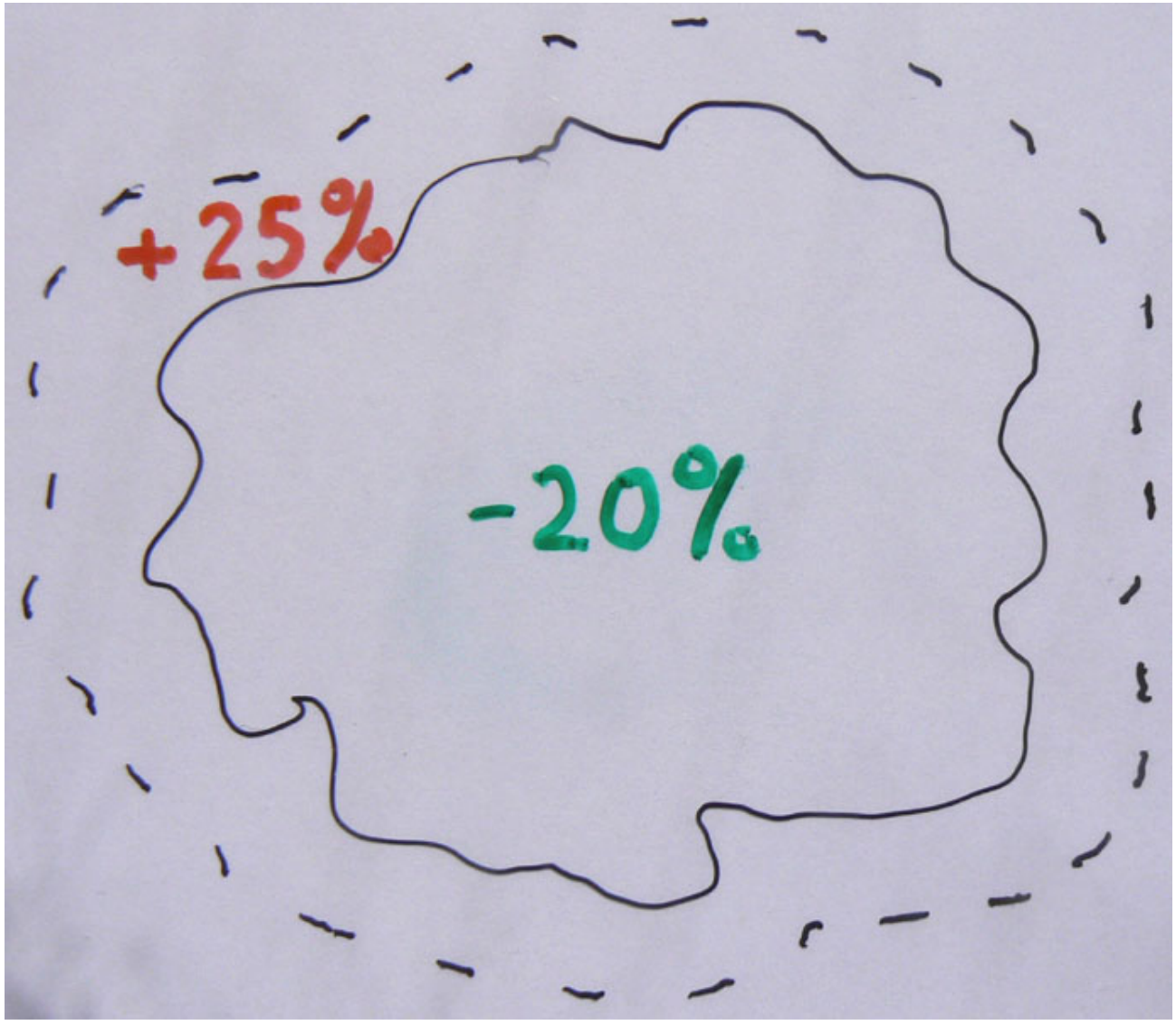
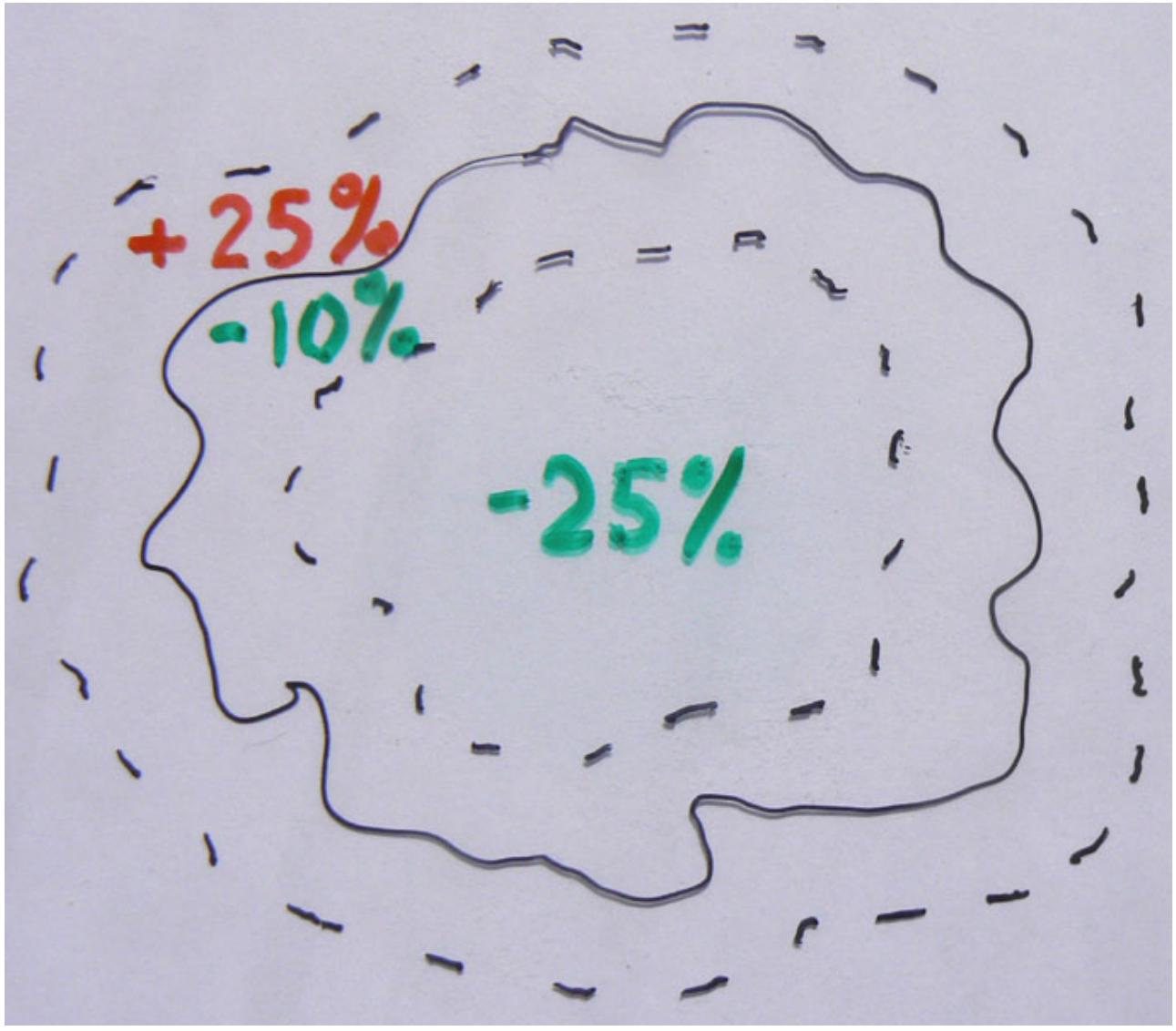
Preliminary results for the proactive part were published in late 2005, showing a significant favourable result, ...

. . . but . . .


+25%
-20%



. . . consistent with the reactive result.

The structuralist ethic

Only trust a model if you

- understand how it was put together
- can test each component

Limits of prediction

Limits of prediction

Avian flu in humans currently has an R_0 of ~ 0.02.

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